

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/553,683  
Source: IFWP  
Date Processed by STIC: 12/14/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 12/14/2006

PATENT APPLICATION: US/10/553,683

TIME: 08:48:28

Input Set : A:\19242.seq.txt

Output Set: N:\CRF4\12142006\J553683.raw

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3 <110> APPLICANT: Hepgenics Pty Ltd
5 <120> TITLE OF INVENTION: VIRAL VECTORS EXPRESSING FUSION OF VIRAL LARGE ENVELOPE
6     PROTEIN AND PROTEIN OF INTEREST
8 <130> FILE REFERENCE: 19242
10 <140> CURRENT APPLICATION NUMBER: 10/553,683
11 <141> CURRENT FILING DATE: 2005-10-17
13 <150> PRIOR APPLICATION NUMBER: AU 2003901876
14 <151> PRIOR FILING DATE: 2003-04-17
16 <160> NUMBER OF SEQ ID NOS: 13
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 25
22 <212> TYPE: DNA
23 <213> ORGANISM: duck
25 <400> SEQUENCE: 1
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31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <400> SEQUENCE: 2
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39 <211> LENGTH: 34
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41 <213> ORGANISM: Homo sapiens
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47 <210> SEQ ID NO: 4
48 <211> LENGTH: 34
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50 <213> ORGANISM: Homo sapiens
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53 ggttgtgatc tagtgctttg ggtgcagtgg cccc                           34
56 <210> SEQ ID NO: 5
57 <211> LENGTH: 3021
58 <212> TYPE: DNA
59 <213> ORGANISM: duck
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62 catgctcatt tgaaagctta tgcaaaaatt aacgaggaat cactggatag ggctaggaga   60
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66 tctcgtttgc gtacttggtt gtcaactcct gagaaatata gaggtagaga tgccccgacc   180
68 attgaagcaa tcactagacc aatccaggtg gctcagggag gcagaaaaac aactacgggt   240

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70 actagaaaac ctcgtggact cgaacctaga agaagaaaag ttaaaaccac agttgtctat 300
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74 cctctcccac gtagttcgag cagccaccat agatctccct cgcctaggaa ataaattacc 420
76 tgctaggcat cacttaggta aattgtcagg actatatcaa atgaagggct gtacttttaa 480
78 ccagaaatgg aaagtaccag atatttcgga tactcatttt aatttagatg tagttaatga 540
80 gtgcccttcc cgaaattgga aatatttgac tccagccaaa ttctggccca agagcatttc 600
82 ctactttcct gtccaggtag gggttaaacc aaagtatcct gacaatgtga tgcaacatga 660
84 atcaatagta ggtaaatatt taaccaggct ctatgaagca ggaatccttt ataagcggat 720
86 atctaaacat ttggtcacat ttaaagggtca gccttataat tgggaacagc aacaccttgt 780
88 caatcaacat cacatttatg atggggcaac atccagcaaa atcaatggac gtcagacgga 840
90 tagaaggagg agaaatactg ttaaaccaac ttgccggaag gatgatccca aaagggactt 900
92 tgacatggtc aggcaagttt ccaacactag atcacgtgtt agaccatgtg caaacaatgg 960
94 aggagataaa caccctccag aatcagggag cttggcctgc tggggcgga aggagagtag 1020
96 gattatcaaa tccgactcct caagagattc ctcagcccca gtggactccc gaggaagacc 1080
98 aaaaagcacg cgaagctttt cgcggttatc aagaagaaag accaccgga accaccacca 1140
100 ttctctcgtc ttccctcctt cagtggaaagc tacaaccggg ggacgatcca ctctgggaa 1200
102 atcagtctct cctcgagact catccgctat accagtcaga accagcgggt ccagtataa 1260
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118 taacgtttgg actttcactt atatggatga ctctctctc tgccacccaa acgctcgtca 1740
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122 ctttgacaaa accacgcctt ctccggtgaa tgaaataaga ttctcgggtt accagattga 1860
124 tgaaaatttc atgaagattg aagaaagcag atggaaagaa ttaaggactg taatcaagaa 1920
126 aataaaaagta ggagaatggt atgactggaa atgtattcaa agatttgtgg ggcatttgaa 1980
128 ttttgttttg ctttttacta aaggtaatat tgaaatgtta aaaccaatgt atgctgctat 2040
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132 aatgggtgtg tgtaaatata gaataaagcc aaagtcctct gtacctttgc cagtgtagc 2160
134 tacagatgct accccaacac atggcgcaat atcccatatc accggcgga gcgcagtgtt 2220
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138 gataatgatt aaaccacgtt gtctcttatc tgattcaact tttgtttgcc ataagcgtaa 2340
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152 ttctttccaa aaatagatga tcttgttaga gatgctaaag acgctttaga gccttattgg 2760
154 aaatcagatt caataaagaa acatgttttg attgcaactc actttgtgga tctcattgaa 2820
156 gacttctggc agactacaca gggcatgcat gaaatagccg aatcattaag agctgttata 2880
158 cctcccacta ctactcctgt tccaccgggt tatcttatcc agcacgagga agctgaagag 2940
160 atacctttgg gagatttatt taaacaccaa gaagaaagga tagtaagttt ccaaccgcac 3000
162 tatccgatta cggctagaat t 3021
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 984

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168 <213> ORGANISM: duck
171 <220> FEATURE:
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (1)..(984)
175 <400> SEQUENCE: 6
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178 1          5          10          15
180 gga gaa ata ctg tta aac caa ctt gcc gga agg atg atc cca aaa ggg      96
181 Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
182          20          25          30
184 act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac     144
185 Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp
186          35          40          45
188 cat gtg caa aca atg gag gag ata aac acc ctc cag aat cag gga gct     192
189 His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala
190          50          55          60
192 tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct     240
193 Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro
194 65          70          75          80
196 caa gag att cct cag ccc cag tgg act ccc gag gaa gac caa aaa gca     288
197 Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala
198          85          90          95
200 cgc gaa gct ttt cgc cgt tat caa gaa gaa aga cca ccg gaa acc acc     336
201 Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr
202          100          105          110
204 acc att cct ccg tct tcc cct cct cag tgg aag cta caa ccc ggg gac     384
205 Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
206          115          120          125
208 gat cca ctc ctg gga aat cag tct ctc ctc gag act cat ccg cta tac     432
209 Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
210          130          135          140
212 cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag     480
213 Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
214 145          150          155          160
216 aaa atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta     528
217 Lys Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu
218          165          170          175
220 ctg gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg     576
221 Leu Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg
222          180          185          190
224 cta gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa     624
225 Leu Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln
226          195          200          205
228 tgc gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga     672
229 Cys Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly
230          210          215          220
232 tct tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt     720

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233 Ser Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu
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236 ttt atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat      768
237 Phe Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr
238                245                250                255
240 ctg acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg      816
241 Leu Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser
242                260                265                270
244 gtc tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg      864
245 Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro
246                275                280                285
248 aaa tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act      912
249 Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr
250                290                295                300
252 tcc tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg      960
253 Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr
254 305                310                315                320
256 ctg tct gct ctt ttt tac aag agt      984
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258                325
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262 <211> LENGTH: 328
263 <212> TYPE: PRT
264 <213> ORGANISM: duck
266 <400> SEQUENCE: 7
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269 1                5                10                15
272 Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
273                20                25                30
276 Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp
277                35                40                45
280 His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala
281                50                55                60
284 Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro
285 65                70                75                80
288 Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala
289                85                90                95
292 Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr
293                100               105               110
296 Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
297                115               120               125
300 Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
301                130               135               140
304 Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
305 145               150               155               160
308 Lys Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu
309                165               170               175
312 Leu Val Ser Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg
313                180               185               190

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316 Leu Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln
317      195      200      205
320 Cys Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly
321      210      215      220
324 Ser Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu
325 225      230      235      240
328 Phe Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr
329      245      250      255
332 Leu Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser
333      260      265      270
336 Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro
337      275      280      285
340 Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr
341      290      295      300
344 Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr
345 305      310      315      320
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349      325
352 <210> SEQ ID NO: 8
353 <211> LENGTH: 501
354 <212> TYPE: DNA
355 <213> ORGANISM: duck
358 <220> FEATURE:
359 <221> NAME/KEY: CDS
360 <222> LOCATION: (1)..(501)
362 <400> SEQUENCE: 8
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364 Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu
365 1      5      10      15
367 gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta      96
368 Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu
369      20      25      30
371 gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc      144
372 Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys
373      35      40      45
375 gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct      192
376 Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser
377      50      55      60
379 tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt      240
380 Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe
381 65      70      75      80
383 atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg      288
384 Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu
385      85      90      95
387 acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc      336
388 Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val
389      100      105      110
391 tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg aaa      384
392 Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys

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**VERIFICATION SUMMARY**

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